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1633

RAW SEQUENCE LISTING

DATE: 01/29/2002

PATENT APPLICATION: US/09/917,376

TIME: 12:18:03

Input Set : A:\401974us.app

Output Set: N:\CRF3\01292002\I917376.raw

PS

3 <110> APPLICANT: DING, SHI-YOU
 4 ADNEY, WILLIAM S.
 5 VINZANT, TODD B.
 6 HIMMEL, MICHAEL E.
 8 <120> TITLE OF INVENTION: THERMAL TOLERANT EXOGLUCANASE FROM ACIDOTHERMUS
 9 CELLULOLYTICUS
 11 <130> FILE REFERENCE: 40197.4US01
 13 <140> CURRENT APPLICATION NUMBER: 09/917,376
 14 <141> CURRENT FILING DATE: 2001-07-28
 16 <160> NUMBER OF SEQ ID NOS: 7
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 957
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Acidothermus cellulolyticus
 25 <220> FEATURE:
 26 <221> NAME/KEY: MOD_RES
 27 <222> LOCATION: (957)
 28 <223> OTHER INFORMATION: Any amino acid
 30 <400> SEQUENCE: 1
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 34 Val Ser Leu Leu Ala Ala Thr Ala Ser Phe Ala Val Ala Ala Ala Leu
 35 20 25 30
 37 Gly Val Leu Pro Ile Ala Ile Thr Ala Ser Pro Ala His Ala Ala Thr
 38 35 40 45
 40 Thr Gln Pro Tyr Thr Trp Ser Asn Val Ala Ile Gly Gly Gly Phe
 41 50 55 60
 43 Val Asp Gly Ile Val Phe Asn Glu Gly Ala Pro Gly Ile Leu Tyr Val
 44 65 70 75 80
 46 Arg Thr Asp Ile Gly Gly Met Tyr Arg Trp Asp Ala Ala Asn Gly Arg
 47 85 90 95
 49 Trp Ile Pro Leu Leu Asp Trp Val Gly Trp Asn Asn Trp Gly Tyr Asn
 50 100 105 110
 52 Gly Val Val Ser Ile Ala Ala Asp Pro Ile Asn Thr Asn Lys Val Trp
 53 115 120 125
 55 Ala Ala Val Gly Met Tyr Thr Asn Ser Trp Asp Pro Asn Asp Gly Ala
 56 130 135 140
 58 Ile Leu Arg Ser Ser Asp Gln Gly Ala Thr Trp Gln Ile Thr Pro Leu
 59 145 150 155 160
 61 Pro Phe Lys Leu Gly Gly Asn Met Pro Gly Arg Gly Met Gly Glu Arg
 62 165 170 175
 64 Leu Ala Val Asp Pro Asn Asn Asp Ile Leu Tyr Phe Gly Ala Pro

ENTERED

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Input Set : A:\401974us.app
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65	180	185	190
67	Ser Gly Lys Gly Leu Trp Arg Ser Thr Asp Ser Gly Ala Thr Trp Ser		
68	195	200	205
70	Gln Met Thr Asn Phe Pro Asp Val Gly Thr Tyr Ile Ala Asn Pro Thr		
71	210	215	220
73	Asp Thr Thr Gly Tyr Gln Ser Asp Ile Gln Gly Val Val Trp Val Ala		
74	225	230	235
76	Phe Asp Lys Ser Ser Ser Leu Gly Gln Ala Ser Lys Thr Ile Phe		
77	245	250	255
79	Val Gly Val Ala Asp Pro Asn Asn Pro Val Phe Trp Ser Arg Asp Gly		
80	260	265	270
82	Gly Ala Thr Trp Gln Ala Val Pro Gly Ala Pro Thr Gly Phe Ile Pro		
83	275	280	285
85	His Lys Gly Val Phe Asp Pro Val Asn His Val Leu Tyr Ile Ala Thr		
86	290	295	300
88	Ser Asn Thr Gly Gly Pro Tyr Asp Gly Ser Ser Gly Asp Val Trp Lys		
89	305	310	315
91	Phe Ser Val Thr Ser Gly Thr Trp Thr Arg Ile Ser Pro Val Pro Ser		
92	325	330	335
94	Thr Asp Thr Ala Asn Asp Tyr Phe Gly Tyr Ser Gly Leu Thr Ile Asp		
95	340	345	350
97	Arg Gln His Pro Asn Thr Ile Met Val Ala Thr Gln Ile Ser Trp Trp		
98	355	360	365
100	Pro Asp Thr Ile Ile Phe Arg Ser Thr Asp Gly Gly Ala Thr Trp [Thr		
101	370	375	380
103	<u>Arg Ile Trp Asp Trp Thr Ser Tyr Pro Asn Arg Ser Leu Arg Tyr Val</u>		
104	385	390	395
106	Leu Asp Ile Ser Ala Glu Pro Trp Leu Thr Phe Gly Val Gln Pro Asn		
107	405	410	415
109	Pro Pro Val Pro Ser Pro Lys Leu Gly Trp Met Asp Glu Ala Met Ala		
110	420	425	430
112	Ile Asp Pro Phe Asn Ser Asp Arg Met Leu Tyr Gly Thr Gly Ala Thr		
113	435	440	445
115	Leu Tyr Ala Thr Asn Asp Leu Thr Lys Trp Asp Ser Gly Gly Gln Ile		
116	450	455	460
118	His Ile Ala Pro Met Val Lys Gly Leu Glu Glu Thr Ala Val Asn Asp		
119	465	470	475
121	Leu Ile Ser Pro Pro Ser Gly Ala Pro Leu Ile Ser Ala Leu Gly Asp		
122	485	490	495
124	Leu Gly Gly Phe Thr His Ala Asp Val Thr Ala Val Pro Ser Thr Ile		
125	500	505	510
127	Phe Thr Ser Pro Val Phe Thr Thr Gly Thr Ser Val Asp Tyr Ala Glu		
128	515	520	525
130	Leu Asn Pro Ser Ile Ile Val Arg Ala Gly Ser Phe Asp Pro Ser Ser		
131	530	535	540
133	Gln Pro Asn Asp Arg His Val Ala Phe Ser Thr Asp Gly Gly Lys Asn		
134	545	550	555
136	Trp Phe Gln Gly Ser Glu Pro Gly Gly Val Thr Thr Gly Gly Thr Val		
137	565	570	575

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Input Set : A:\401974us.app
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139 Ala Ala Ser Ala Asp Gly Ser Arg Phe Val Trp Ala Pro Gly Asp Pro
140 580 585 590
142 Gly Gln Pro Val Val Tyr Ala Val Gly Phe Gly Asn Ser Trp Ala Ala
143 595 600 605
145 Ser Gln Gly Val Pro Ala Asn Ala Gln Ile Arg Ser Asp Arg Val Asn
146 610 615 620
148 Pro Lys Thr Phe Tyr Ala Leu Ser Asn Gly Thr Phe Tyr Arg Ser Thr
149 625 630 635 640
151 Asp Gly Gly Val Thr Phe Gln Pro Val Ala Ala Gly Leu Pro Ser Ser
152 645 650 655
154 Gly Ala Val Gly Val Met Phe His Ala Val Pro Gly Lys Glu Gly Asp
155 660 665 670
157 Leu Trp Leu Ala Ala Ser Ser Gly Leu Tyr His Ser Thr Asn Gly Gly
158 675 680 685
160 Ser Ser Trp Ser Ala Ile Thr Gly Val Ser Ser Ala Val Asn Val Gly
161 690 695 700
163 Phe Gly Lys Ser Ala Pro Gly Ser Ser Tyr Pro Ala Val Phe Val Val
164 705 710 715 720
166 Gly Thr Ile Gly Gly Val Thr Gly Ala Tyr Arg Ser Asp Asp Cys Gly
167 725 730 735
169 Thr Thr Trp Val Leu Ile Asn Asp Asp Gln His Gln Tyr Gly Asn Trp
170 740 745 750
172 Gly Gln Ala Ile Thr Gly Asp His Ala Asn Leu Arg Arg Val Tyr Ile
173 755 760 765
175 Gly Thr Asn Gly Arg Gly Ile Val Tyr Gly Asp Ile Gly Gly Ala Pro
176 770 775 780
178 Ser Gly Ser Pro Ser Pro Ser Val Ser Pro Ser Ala Ser Pro Ser Leu
179 785 790 795 800
181 Ser Pro Ser Pro Ser Pro Ser Ser Pro Ser Pro Ser Pro Ser Pro
182 805 810 815
184 Ser Ser Ser Pro Ser Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro
185 820 825 830
187 Ser Pro Ser Arg Ser Pro Ser Pro Ser Ala Ser Pro Ser Pro Ser Ser
188 835 840 845
190 Ser Pro Ser Pro Ser Ser Pro Ser Ser Ser Pro Ser Pro Thr Pro
191 850 855 860
193 Ser Ser Ser Pro Val Ser Gly Gly Val Lys Val Gln Tyr Lys Asn Asn
194 865 870 875 880
196 Asp Ser Ala Pro Gly Asp Asn Gln Ile Lys Pro Gly Leu Gln Val Val
197 885 890 895
199 Asn Thr Gly Ser Ser Ser Val Asp Leu Ser Thr Val Thr Val Arg Tyr
200 900 905 910
202 Trp Phe Thr Arg Asp Gly Gly Ser Ser Thr Leu Val Tyr Asn Cys Asp
203 915 920 925
205 Trp Ala Ala Ile Gly Cys Gly Asn Ile Arg Ala Ser Phe Gly Ser Val
206 930 935 940
208 Asn Pro Ala Thr Pro Thr Ala Asp Thr Tyr Leu Gln Xaa
209 945 950 955
212 <210> SEQ ID NO: 2

W-
X

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/917,376

DATE: 01/29/2002
TIME: 12:18:03

Input Set : A:\401974us.app
Output Set: N:\CRF3\01292002\I917376.raw

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213 <211> LENGTH: 2869
214 <212> TYPE: DNA
215 <213> ORGANISM: Acidothermus cellulolyticus
217 <220> FEATURE:
218 <221> NAME/KEY: modified_base
219 <222> LOCATION: (2869)
220 <223> OTHER INFORMATION: a, c, t, g, other or unknown
222 <400> SEQUENCE: 2
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224 gcccgcactg cgtcgttcgc cgtggccgcc gctctggag ttctgccccat cgcgataacg 120
225 gcttcctcctg cgcacgcggc gacgacttagt ccgtacacct ggagcaacgt ggcatcggtt 180
226 ggccggcggtt ttgtcgacgg gatcgcttc aatgaagggtt caccggaaat tctgtacgtt 240
227 cggacggaca tcggggggat gtatcgatgg gatgccgc a cggccgggtt gatccctt 300
228 ctggattggg tggatggaa caattggggg tacaacggcg tcgtcagcat tgccgcagac 360
229 cccatcaata ctaacaaggat atggccgc gtcggaaatgtt acaccaacag ctgggaccac 420
230 aacgacggag cgattctcg ctcgtctgtt cagggcgcaa cgtggcaaat aacgccccctg 480
231 ccgttcaagc ttggccgc aa catgcccggg cgtggaaatgg gcgagcggct tgcgggtggat 540
232 ccaaacaatg acaacattct gtatccggc gccccgagcg gcaaagggtt ctggagaagc 600
233 acagattccg gcgcgacactg gtcccgatgtt acgaacttcc cggacgttgg cactgtacatt 660
234 gcaaatccca ctgacacgc cggctatctt agcgatattt aaggcgctgt ctgggtcgct 720
235 ttgcacaagt cttcgatcatc gctccggccaa gcgagtaaga ccattttgtt gggcgtggcg 780
236 gatcccaata atccggctt ctggagcaga gacggccggc cgcacgtggca ggccgtgcgg 840
237 ggtcgccga cccgttcat cccgcacaag ggcgtttt acccggttcaa ccaacgtgctc 900
238 tatattgcca ccagcaatac ggggtgtccg tatgacgggaa gtcggccgaa cgtctggaaa 960
239 ttctcggtga ctcggggac atggacgcga atcagccggg taccttgcac ggacacggcc 1020
240 aacgactact ttggttacag cggcctcaat atcgaccgc agcaccggaa cactgtatg 1080
241 gtggcaaccc agatatcggtt gtggccggac accataatctt ttcggagcac cgacggcggt 1140
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243 cttgacattt cggcggagcc ttggctgacc ttcggctgttcc agccgaatcc tcccgatacc 1260
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246 ggccggccaga ttcatatcgc gccatggtc aaaggattgg aggagacggc ggttaacgat 1440
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248 acccacgccc acgttactgc cgtgccatcg acgatcttca cgtcacgggtt gttcacgacc 1560
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253 ggatttggca actccctggc tgcgtcgaa ggtgttcccg ccaatgcctt gatccgtctc 1860
254 gaccgggtga atccaaagac tttctatgcc ctatccaatg gAACCTTCA tcaagacacg 1920
255 gacggccggc tgacattcca accggtcgcg gccggcttc cggcagcgg tgcgtcggt 1980
256 gtcatgttcc acgcgggttcc tggaaaagaa ggcgatctgtt ggctcgctgc atcgagcggg 2040
257 ctttaccact caaccaatgg cggcagcgtt gggtctgttcc tcaaccggctt atccctccgc 2100
258 gtgaacgtgg gatggtaat gtcgtcgccc ggggtctgtt acccagccgtt ctttgcgtt 2160
259 ggcacgatcg gaggcggttac gggggcgatc cgcgtccgacg actgtggac gacgtgggtt 2220
260 ctgtatcaatg atgaccagca ccaatacgaa aattggggac aagcaatcac cggtgaccac 2280
261 gcaatttac ggcgggttca cataggcaccg aacggccgtt gaaattgtata cggggacattt 2340
262 ggtgtcgcc cgtccggatc gccgtctccg tcgggtgatc cgtcggttcc gccgagcctt 2400
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/917,376

DATE: 01/29/2002
TIME: 12:18:03

Input Set : A:\401974us.app
Output Set: N:\CRF3\01292002\I917376.raw

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 265 tcggcgtcgc cgagccggtc ttgcgtaccg agcccgctt cgtcaccgtc ttgcgtcgccg 2580
 266 agcccaacgc cgtcggtcgc gccgggtgtcg ggtgggtga aggtgcagta taagaataat 2640
 267 gattcggtcgc cgggtgataa tcagatcaag ccgggtttgc aggtgggtaa taccgggtcg 2700
 268 tcgtcggtgg atttgcgtcgc ggtgacgggt cggtactgggt tcacccggga tggtggtcg 2760
 269 tcgacactgg tgtacaactg tgactgggtcgc gcatcggt gtggaaatcccgccctcg 2820
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 274 <211> LENGTH: 740
 275 <212> TYPE: PRT
 276 <213> ORGANISM: Acidothermus cellulolyticus
 278 <220> FEATURE:
 279 <223> OTHER INFORMATION: Catalytic domain GH74
 281 <400> SEQUENCE: 3
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 283 1 5 10 15
 285 Gly Phe Val Asp Gly Ile Val Phe Asn Glu Gly Ala Pro Gly Ile Leu
 286 20 25 30
 288 Tyr Val Arg Thr Asp Ile Gly Gly Met Tyr Arg Trp Asp Ala Ala Asn
 289 35 40 45
 291 Gly Arg Trp Ile Pro Leu Leu Asp Trp Val Gly Trp Asn Asn Trp Gly
 292 50 55 60
 294 Tyr Asn Gly Val Val Ser Ile Ala Ala Asp Pro Ile Asn Thr Asn Lys
 295 65 70 75 80
 297 Val Trp Ala Ala Val Gly Met Tyr Thr Asn Ser Trp Asp Pro Asn Asp
 298 85 90 95
 300 Gly Ala Ile Leu Arg Ser Ser Asp Gln Gly Ala Thr Trp Gln Ile Thr
 301 100 105 110
 303 Pro Leu Pro Phe Lys Leu Gly Gly Asn Met Pro Gly Arg Gly Met Gly
 304 115 120 125
 306 Glu Arg Leu Ala Val Asp Pro Asn Asn Asp Asn Ile Leu Tyr Phe Gly
 307 130 135 140
 309 Ala Pro Ser Gly Lys Gly Leu Trp Arg Ser Thr Asp Ser Gly Ala Thr
 310 145 150 155 160
 312 Trp Ser Gln Met Thr Asn Phe Pro Asp Val Gly Thr Tyr Ile Ala Asn
 313 165 170 175
 315 Pro Thr Asp Thr Thr Gly Tyr Gln Ser Asp Ile Gln Gly Val Val Trp
 316 180 185 190
 318 Val Ala Phe Asp Lys Ser Ser Ser Ser Leu Gly Gln Ala Ser Lys Thr
 319 195 200 205
 321 Ile Phe Val Gly Val Ala Asp Pro Asn Asn Pro Val Phe Trp Ser Arg
 322 210 215 220
 324 Asp Gly Gly Ala Thr Trp Gln Ala Val Pro Gly Ala Pro Thr Gly Phe
 325 225 230 235 240
 327 Ile Pro His Lys Gly Val Phe Asp Pro Val Asn His Val Leu Tyr Ile
 328 245 250 255
 330 Ala Thr Ser Asn Thr Gly Gly Pro Tyr Asp Gly Ser Ser Gly Asp Val
 331 260 265 270
 333 Trp Lys Phe Ser Val Thr Ser Gly Thr Trp Thr Arg Ile Ser Pro Val

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/917,376

DATE: 01/29/2002

TIME: 12:18:04

Input Set : A:\401974us.app

Output Set: N:\CRF3\01292002\I917376.raw

L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4